

Figure 1

Light chain sequences

1	10	20	30	40	
EIVLTQSPGTL SLSPGERATL SCRASQSVSSSYLAWYQQK					germ-line
EIVLTQSPGTL SLSPGERATL SCRASQSVSSSFLAWYQQK					(1) AB1
ENVLTQSPGTL SLSPGERATL SCRASQSGSSSYLAWYQQK					(1) AB7
EIVLTQSPGTL SLSPGERATL SCRASQSVSSSFLAWYQQK					(1) AB11
EIVLTQSPGTL SLSPGERATL SCRASQSVSS-YLAWYQQK					(1) AB12
41	50	60	70	80	
PGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLE					germ-line
PGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLE					(41) AB1
PGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLE					(41) AB7
PGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLE					(41) AB11
PGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLE					(41) AB12
81	90	100	110	120	
PEDFAVYYCQQYGSSP-----					germ-line
PEDFAVYYCQQYSSSPLTFGGGTKVEIKRTVAAPSVFIFP					(81) AB1
PEDFAVYYCQQYGSSPITFGQGTRLEIKRTVAAPSVFIFP					(81) AB7
PEDFAVYYCQQYSSSPLTFGGGTKVEIKRTVAAPSVFIFP					(81) AB11
PEDFAVYYCQQYGSSPLTFGGGTKVEIKRTVAAPSVFIFP					(81) AB12

CDR1, CDR2, and CDR3 have been underlined.

Figure 2

Heavy chain sequences

1	10	20	30	40	
QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQA					germ-line
QVQLVQSGAEVKKPGSSVKVSCKASGGTFSRYPINWVRQA					(1) AB1
QVQLVQSGAEVKKPGSSVKVSCKASGGTFSRYAINWVRQA					(1) AB7
QVQLVQSGAEVKKPGSSVKVSCKASGGTFSRYPINWVRQA					(1) AB11
QVQLVQSGAEVKKPGSSVKVSCKASGGTFSRYIINWVRQA					(1) AB12
41	50	60	70	80	
PGQGLEWMGRIIPILGIANYAQKFQGRVTITADKSTSTAY					germ-line
PGQGLEWMGRIIPILGIADYAQRFQGRVTITADKSTNTAY					(43) AB1
PGQGLEWMGRIIPILDIADYAQKFQDRVTITADKSTNTAY					(43) AB7
PGQGLEWMGRIIPILGIADYAQRFQGRVTITADKFTNTAY					(43) AB11
PGQGLEWMGRIIPILGVENYAQKFQGRVTITADKSTSTAY					(43) AB12
81	90	100	110	120	
MELSSLRSED TAVYYCAR -----					germ-line
MELSSLRSED TAVYYCARRDWG DYWGQGLVTVSSASTKG					(85) AB1
MELSSLRSED TAVYYCARKDW FDYPWGQGLVTVSSASTKG					(85) AB7
MELSSLRSED TAVYYCARRDWG DYWGQGLVTVSSASTKG					(85) AB11
MELSSLRSED TAVYYCARKDW FDYWGQGLVTVSSASTKG					(85) AB12
121					
-----		germ-line			
PSVFPLA		(121) AB1			
PSVFPLA		(121) AB7			
PSVFPLA		(121) AB11			
PSVFPLA		(121) AB12			

CDR1, CDR2, and CDR3 regions have been underlined.

Figure 3

VHABlnoleader

	ABs2	FR1
+1	Q V Q L V Q S G A E V K K P G S S V K V	
1	CAGTTTCAGC TGCTGCAGTC TGGGCTGAG GTGAAGAAGC CTGGCTCCTC GGTGAAGTC	
	FR1	FR2
+1	S C K A S G G T F S R Y P I N W V R Q A	CDR1
61	TCCTGCAAG CTCTTGAGG CACCTTCAGC CGTTATCCTA TCAACTGGGT GCGACAGGCC	
	FR2	CDR2
+1	P G Q G L E W M G R I I P I L G I A D Y	
121	CCTGACAAG GCCTTGAGTG GATGGAGAG ATCATCCCTA TCCTTGTAT AGCAGACTAC	
	CDR2	FR3
+1	A Q R F Q G R V T I T A D K S T N T A Y	
181	GCACAGAGT TCCAGGGCAG AGTCACGATT ACCGGGACA AATCCACGAA CACAGCCTAC	
	FR3	CDR3
+1	M E L S S L R S E D T A V Y Y C A R R D	JH4b
241	ATGAGCTGA GCAGCCTGAG ATCTGAGGAC ACGGCCGTGT ATTATTTGTC GAGGAGGGAC	
	CDR3	gamma-1 constant
	FR4	
+1	W G D Y W G Q G T L V T V S S A S T K G	JH4b
301	TGGGAGACT ACTGGGGCCA GGAACCTG GTACCGTCT CCTCAGCCTC CACCAAGGC	
	ABs0	
	gamma-1 constant	
+1	P S V F P L A	
361	CCATCGGTCT TCCCCCTGGC A	

Figure 4

VLBIwihleader

		AB125		leader	
+1	M E A P A Q L L F L L L W L P D T T G				
1	ATGGAAGCCC CAGCACAGCT TCCTCTCCCTC CTGCTACTCT GGTCCACAGA TACCACCGGA				
		AB11		FR1	
+1	E I V L T Q S P G T L S L S P G E R A T				
61	GAAATTGTGT TGACGCAGTC TTCAGGCACC CTGTCTTGT CTCACGGGA AAGAGCCACC				
		FR1		CDR1	
+1	L S C R A S Q S V S S S F L A W Y Q Q K				
121	CTCTCCTGCA GGGCCAGTCA GAGTGTAGC AGCAGCTCT TAGCCTGTA CCAGCAGAAA				
		FR2		CDR2	
+1	P G Q A P R L L I Y G A S S R A T G I P				
181	CCTGGCCAGG CTCCACAGCT CCTCATCTAT GTGCATCCA GCAGGGCCAC TGGCATCCCA				
		FR3		CDR3	
+1	D R F S G S G T D F T L T I S R L E				
241	GACAGGTCA GTGGCAGTGG GTCTGGGACA GACTCACTC TCACCATCAG CAGACTGGAG				
		FR3		CDR3	
+1	P E D F A V Y Y C Q Q Y S S S P L T F G				
301	CCTGAAGATT TTGCAGTGTA TTACTGTCAG CAGTATAGTA GCTCACCGCT CACTTTGCGC				
		FR4		CDR4	
+1	G G T K V E I K R T V A A P S V F I F P				
361	GGAGGACCA AGGTGAGAT CAAACGAAT GTGCTGCAC CATCTGTCTT CATCTCCCG				
		JK4		kappa constant	
		AB16		FR4	

Figure 5

VHAB7noleader

	AB62		FR1	
+1	Q V Q L V Q S G A E V K K P G S S V K V			
1	CAGGTTCAGC TGGTCAGTC TGGGCTGAG GTGAGAAGC CTGGTCCTC GGTGAAGTC			
	FR1			FR2
+1	S C K A S G G T F S R Y A I N W V R Q A	CDR1		
61	TCCTGCAAGG CTCTGAGG CACCTTCAGC AGATATGCTA TCAACTGGGT GCGACAGGCC			
	FR2			CDR2
+1	P G Q G L E W M G R I I P I L D I A D Y			
121	CCTGGACAAG GACTTGAGTG GATGGAAGG ATCATCCCTA TCCTGATAT AGCAGACTAC			FR3
	CDR2			
+1	A Q K F Q D R V T I T A D K S T N T A Y			
181	GCACAGAAGT TCCAGGACAG AGTCACGATP ACCGGGACA AGTCCACGAA CACAGCCTAC			CDR3
				JH5b
+1	M E L S S L R S E D T A V Y C A R K D	FR3		
241	ATGGAGCTGA GCAGCCTGAG ATCTGAGGAC ACGGCCGTGT ATTACTGTGC GAGAAAGGAC		FR4	
	CDR3			gamma-1 constant
		JH5b		
+1	W F D P W G Q G T L V T V S S A S T K G			
301	TGGTTGACC CTTGGGGCCA GGAACCTTG GTACCCGTCT CTTCAACCTC CACCAAGGC			
	gamma-1 constant			
	AB90			
+1	P S V F P L A			
361	CCATCGGTCT TCCCCCTGGC A			

Figure 6

VLAB7wihthead

		leader	
		AB125	
+1	M E A P A Q L L F L L L W L P D I T G		
1	ATGGAAGCCC CAGACAGCT TCTCTCCCT CTGCTACTCT GGTCCCGA TATCACCGGA		
		FR1	
+1	E N V L T Q S P G T L S L S P G E R A T		
61	GAAATGTGT TGAAGCAGTC TCCAGGACC CTGTCTGT CTCCAGGGGA AAGAGCCACC		
		FR2	
+1	L S C R A S Q S G S S Y L A W Y Q Q K	CDR1	
121	CTCTCTGCA GGGCCAGTCA GAGTGTAAC AGCAGTACT TAGCTGTGTA CCAGAGAAA		
		FR3	
+1	P G Q A P R L L I Y G A S S R A T G I P	CDR2	
181	CCTGGCCAGG CTCCAGGCT CCTCATCTAT GTGCAATCCA GTAGGCCAC TGGCATCCCA		
		FR4	
+1	D R F S G S G S G T D F T L T I S R L E	CDR3	
241	GACAGTCA GTGGCAGTGG GTCTGGACA GACTCACTC TCACCATCAG CAGACTGGAG		
		FR5	
+1	P E D F A V Y Y C Q Q Y G S S P I T F G	CDR4	
301	CCTGAGATT TTGCAAGTGA TTAAGTCAAG CAGTAAGTGA GTTCACCGAT CACCTTCGGC		
		FR6	
+1	Q G T R L E I K R T V A A P S V F I F P	CDR5	
361	CAAGGACAC GACTGAGAT TAAAGAACT GTGCTGCAC CAATGTCTT CATCTTCCCC		

Figure 7

VHAB1no1leader

		FR1	
		AB62	
+1	Q V Q L V Q S G A E V K K P G S S V K V		
1	CAGGTGCAGC TGGTCAGTC TGGGGCTGAG GTGAGAAGC CTGGGTCTTC GGTGAAGTC		
		FR1	FR2
+1	S C K A S G G T F S R Y P I N W V R Q A	CDR1	
61	TCCTGCAAGG CTCTGAGG CACCTTCAGC CGTTATCCTA TCACTGGGT GCGACAGGCC		
		FR2	CDR2
+1	P G Q G L E W M G R I I P I L G I A D Y		
121	CCTGGACAAG GCCTTGAGTG GATGGAGAAG ATCATCCCTA TCCTTGATAT AGCAGACTAC		
		CDR2	FR3
+1	A Q R F Q G R V T I T A D K F T N T A Y		
181	GCACAGAGGT TCCAGGGCAG AGTCAGATT ACCGCGACA AATTCAGAA CACAGCCTAC		
		CDR3	D7-27
+1	M E L S S L R S E D T A V Y Y C A R R D	FR3	CDR3
241	ATGGAGCTGA GCAGCCTGAG ATCTGAGGAC ACGGCCGTGT ATTATTGTGC GAGGAGGAC	JH4b	
		CDR3	gamma-1'constant
		D7-27	FR4
+1	W G D Y W G Q G T L V T V S S A S T K G	JH4b	
301	TGGGAGACT ACTGGGGCCA GGGAACCTTG GTCACCGTCT CCTCAGCCTC CACCAAGGC		
		gamma-1'constant	
		AB90	
+1	P S V F P L A		
361	CCATCGGTCT TCCCCCTGGC A		

Figure 8

VLAB1withleader

leader	
	AB125
+1	M E A P A Q L L F L L L W L P D T T G
1	ATGGAAGCCC CAGCACAGCT TCTCTTCCTC CTGCTACTCT GGCCTCCAGA TACCACCGGA
FR1	
+1	E I V L T Q S P G T L S L S P G E R A T
61	GAATGTGT TGACGACATC TCCAGGCACC CTGCTTTGT CTCGAGGGA AAGAGCCACC
FR2	
+1	L S C R A S Q S V S S S F L A W Y Q Q K
121	CTCTCCTGCA GGGCCAGTCA GAGTGTAGC AGCAGCTCT TAGCCTGTA CCAGCAGAAA
FR3	
+1	P G Q A P R L L I Y G A S S R A T G I P
181	CCTGGCCAGG CTCCCAGGCT CCTCATCTAT GGTGCATCCA GCAGGGCCAC TGGCATCCCA
FR4	
+1	D R F S G S G T D F T L T I S R L E
241	GACAGGTCA GTGGCAGTGG GTCTGGGACA GACTCACTC TCACCATCAG CAGACTGGAG
FR5	
+1	P E D F A V Y Y C Q Q Y S S S P L T F G
301	CCTGAAGATT TTGCAGTGT TTA CTGTGAG CAGTATAGTA GCTCACCCT CACTTTGGC
FR6	
+1	G G T K V E I K R T V A A P S V F I F P
361	GGAGGACCA AGGTGAGAT CAAACGACT GTGCTGCAC CATCTGTCTT CATCTTCCCC
421	G

Figure 9

VHAB12noleader

AB63	
	FR1
+1	Q V Q L V Q S G A E V K K P G S S V K V
1	CAGTGCCAGC TGGTGCAATC TGGGGCTGAG GTGAAGAAGC CTGGGTCCTC GGTGAAGTTC
FR1	
	CDR1
+1	S C K A S G G T F S R Y I I N W V R Q A
61	TCCTGCAAGG CTTCTGAGG CACCTTCAGC AGTATATTA TCAACTGGGT GCGACAGGCC
FR2	
	CDR2
+1	P G Q G L E W M G R I I P I L G V E N Y
121	CCTGACAAG GCTTGAGTG GATGGAAGG ATCATCCCTA TCCTTGTGT AGAAACTTAC
FR3	
	CDR2
+1	A Q K F Q G R V T I T A D K S T S T A Y
181	GCACAGAAGT TCCAGGGCAG AGTCACGATT ACCGCGACA AATCCAGAG CACAGCCTAC
FR3	
	CDR3
+1	M E L S S L R S E D T A V Y Y C A R K D
241	ATGAGCTGA GCAGCTGAG ATCTGAGAGC ACGGCCGTGT ATTACTGTGC GAGAAAGGAC
FR4	
	gamma-1constant
	JH4b
+1	W F D Y W G Q G T L V T V S S A S T K G
301	TGGTTGATTT ACTGGGGCCA GGAACCTG GTCAACCTCT CCTCAGCCTC CACCAAGGGC
AB90	
	gamma-1constant
	JH4b
+1	P S V F P L A
361	CCATCGTCT TCCCCCTGC A

Figure 10

VLAB12noleader

	AB125	leader	
+1	M E A P A Q L L F L L L W L P D T T G		
1	ATGAAGCCC CAGCAGAGCT TCTCTTCCTC CTGCTACTCT, GGCTCCAGGA TACCACCGA		
		FR1	
+1	E I V L T Q S P G T L S L S P G E R A T		
61	GAAATGTGT TGACGAGTC TCCAGGCACC CTGTCTTTGT CTCAGGGGA AAGAGCCACC		
		FR1	
		CDR1	
+1	L S C R A S Q S V S S Y L A W Y Q Q K P		
121	CTCTCTGCA GGGCCAGTCA GAGTGTAGC AGCTACTTAG CCTGGTACCA GCAGAAACCT		
		FR2	
		CDR2	
+1	G Q A P R L L I Y G A S S R A T G I P D		
181	GGCCAGGCTC CCAGGCTCCT CATCTATGCT GCATCCAGCA GGGCCACTGG CATCCAGAC		
		FR3	
		CDR3	
+1	R F S G S G S G T D F T L T I S R L E P		
241	AGTTCACTG GCAGTGGGTC TGGACAGAC TTCACCTTCA CCATCAGCAG ACTGAGACCT		
		FR4	
		JK4	
+1	E D F A V Y Y C Q Q Y G S S P L T F G G		
301	GAAGATTTG CAGTGTATTA CTGTACGACG TATGTAGCT CACCGCTCAC TTTCGGCGGA		
		FR4	
		AB16	
		Kappa constant	
+1	G T K V E I K R T V A A P S V F I F P		
361	GGGACCAAGG TGGAGATCAA ACGAACTGTG GCTGCACCAT CTGTCTTCAT CTTCGCCG		

Figure 11

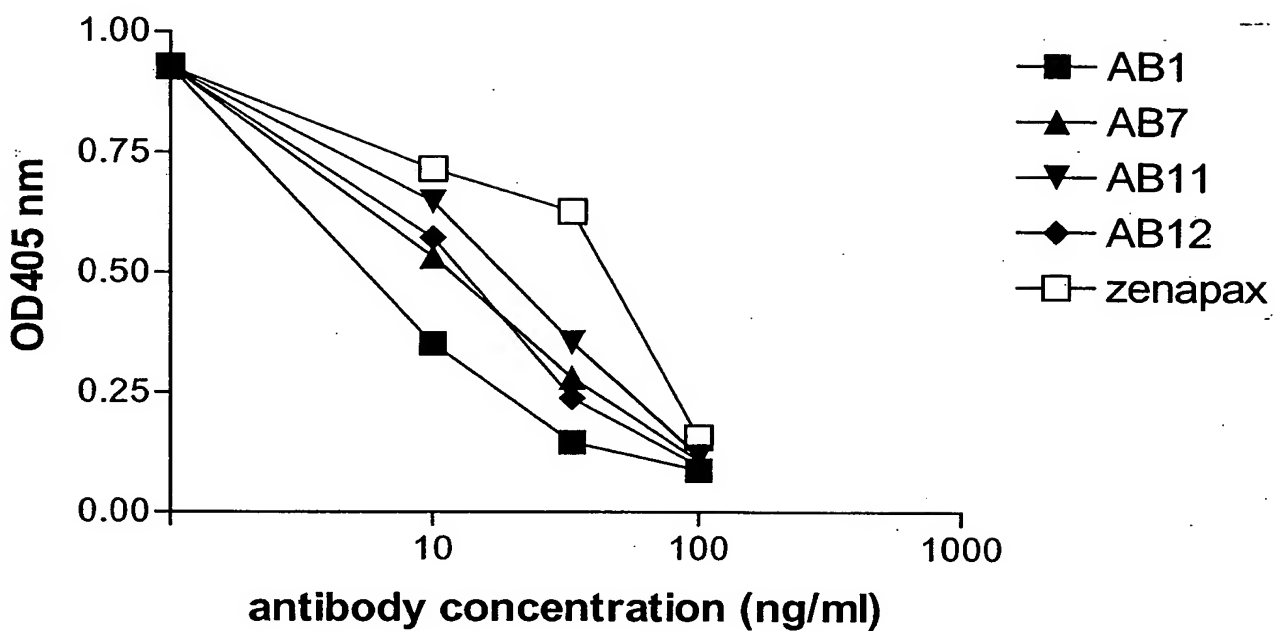


Figure 12

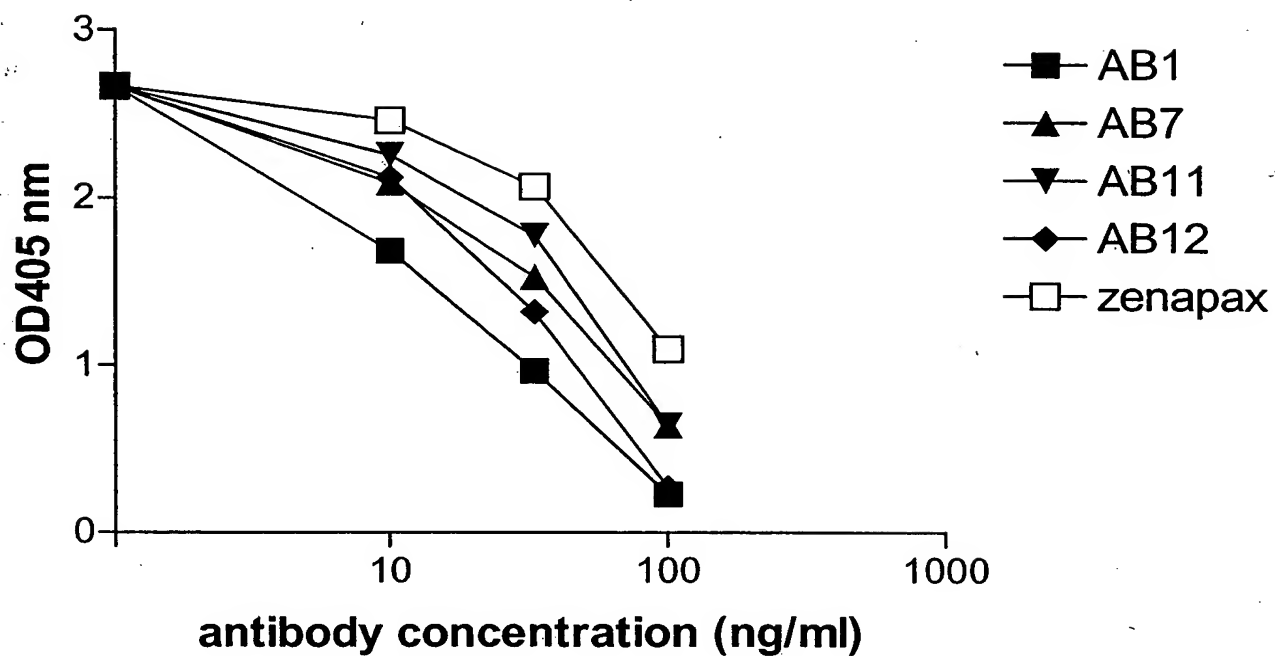


Figure 13

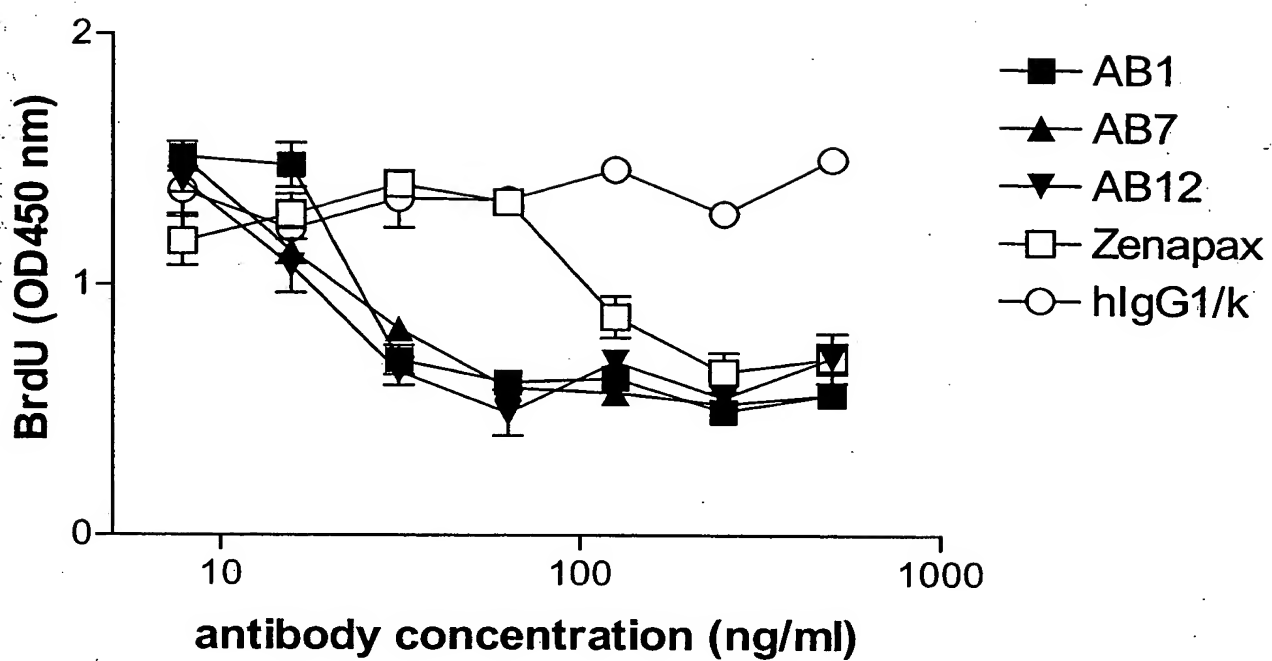


Figure 14

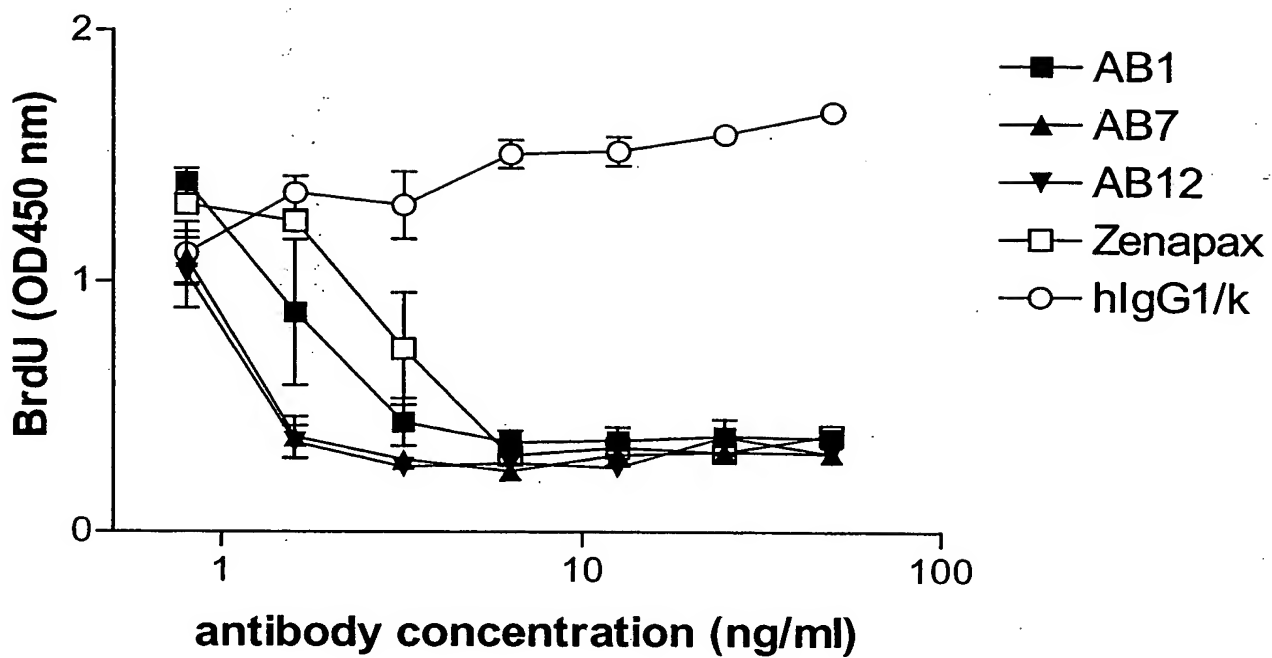


Figure 15

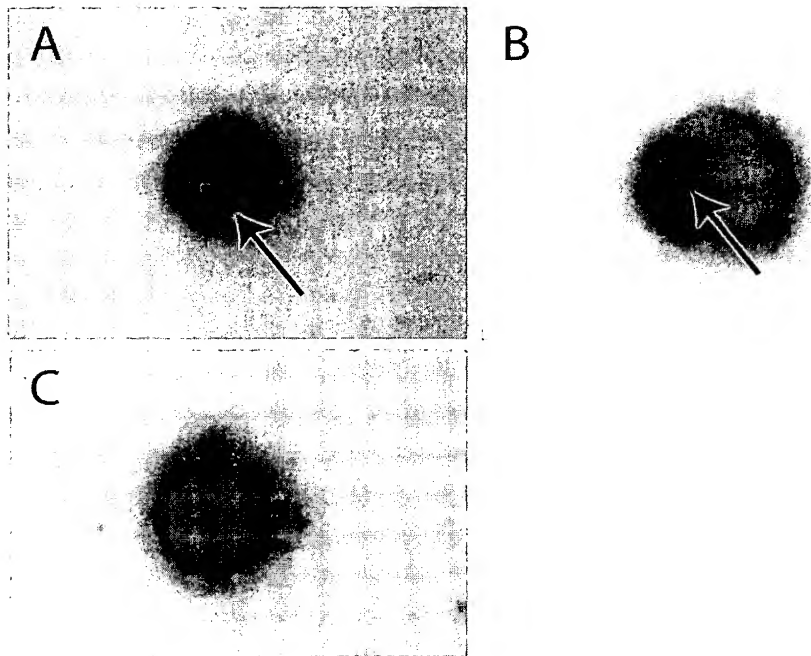
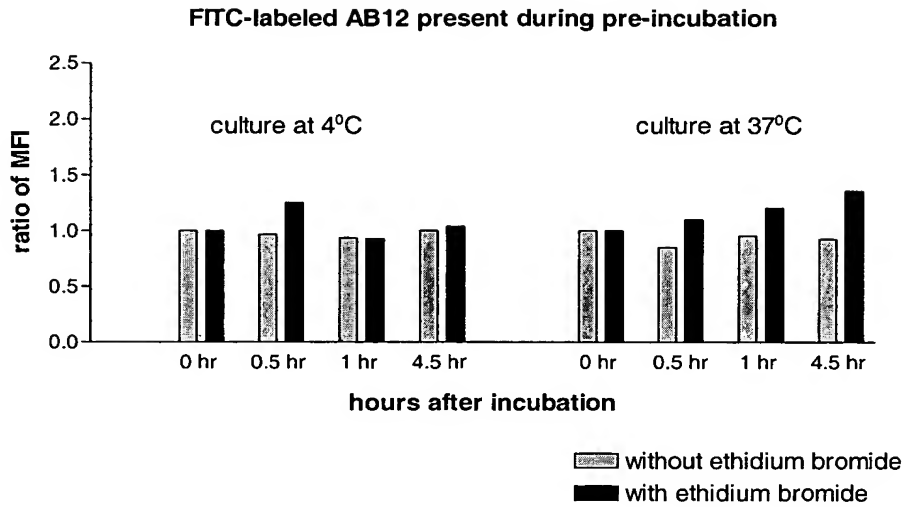


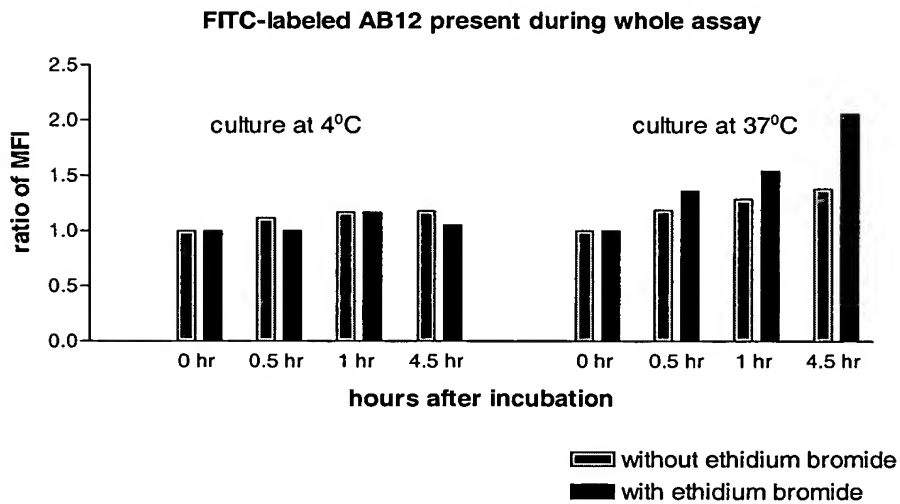
Figure 16

A



5

B



10